

FIG. 1

BEST AVAILABLE COPY

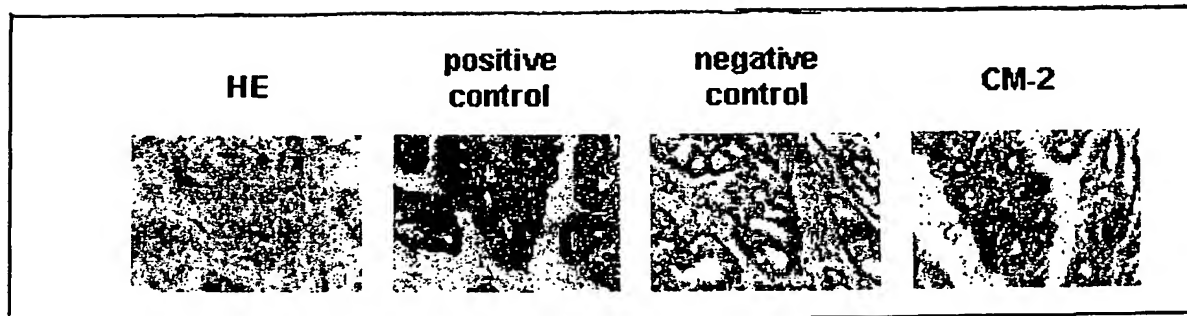


FIG. 2

BEST AVAILABLE COPY

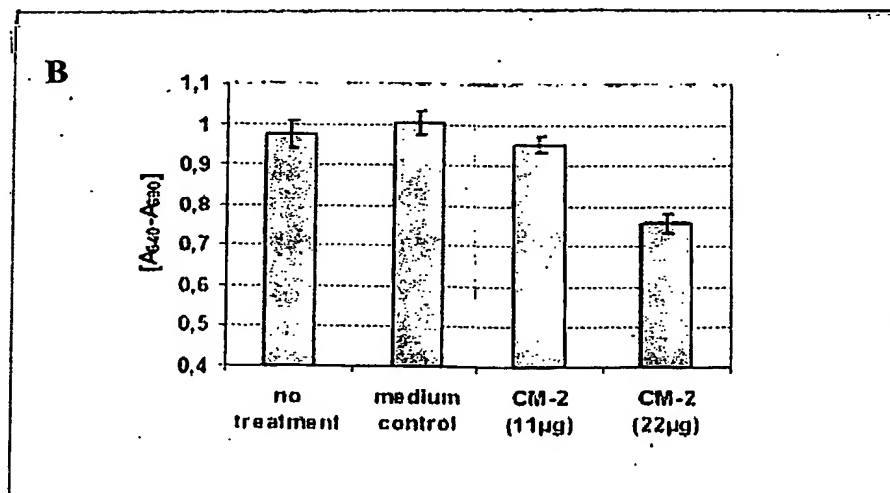
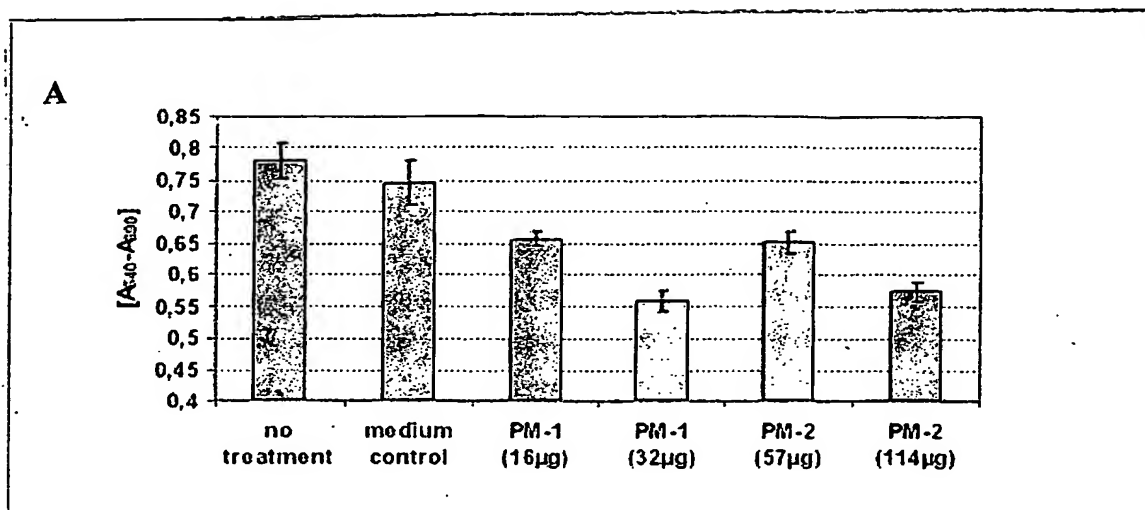


FIG. 3

BEST AVAILABLE COPY

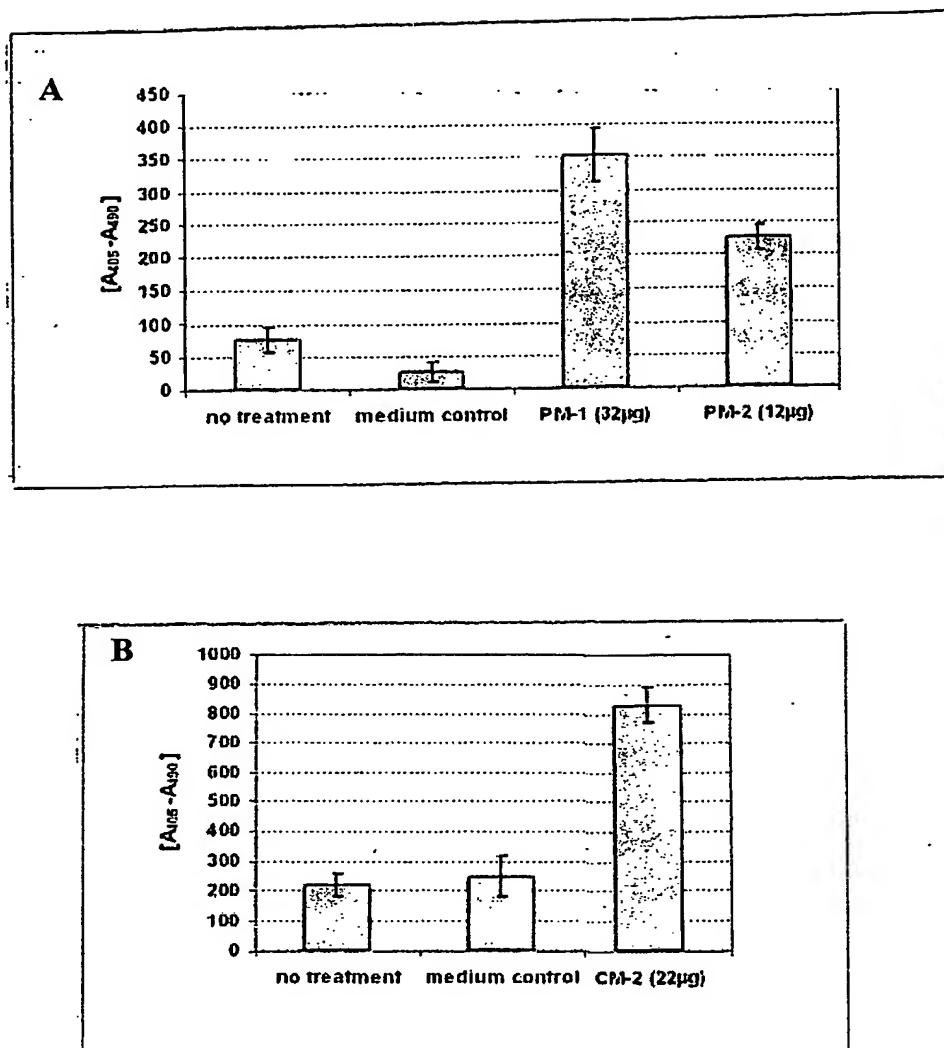


FIG. 4

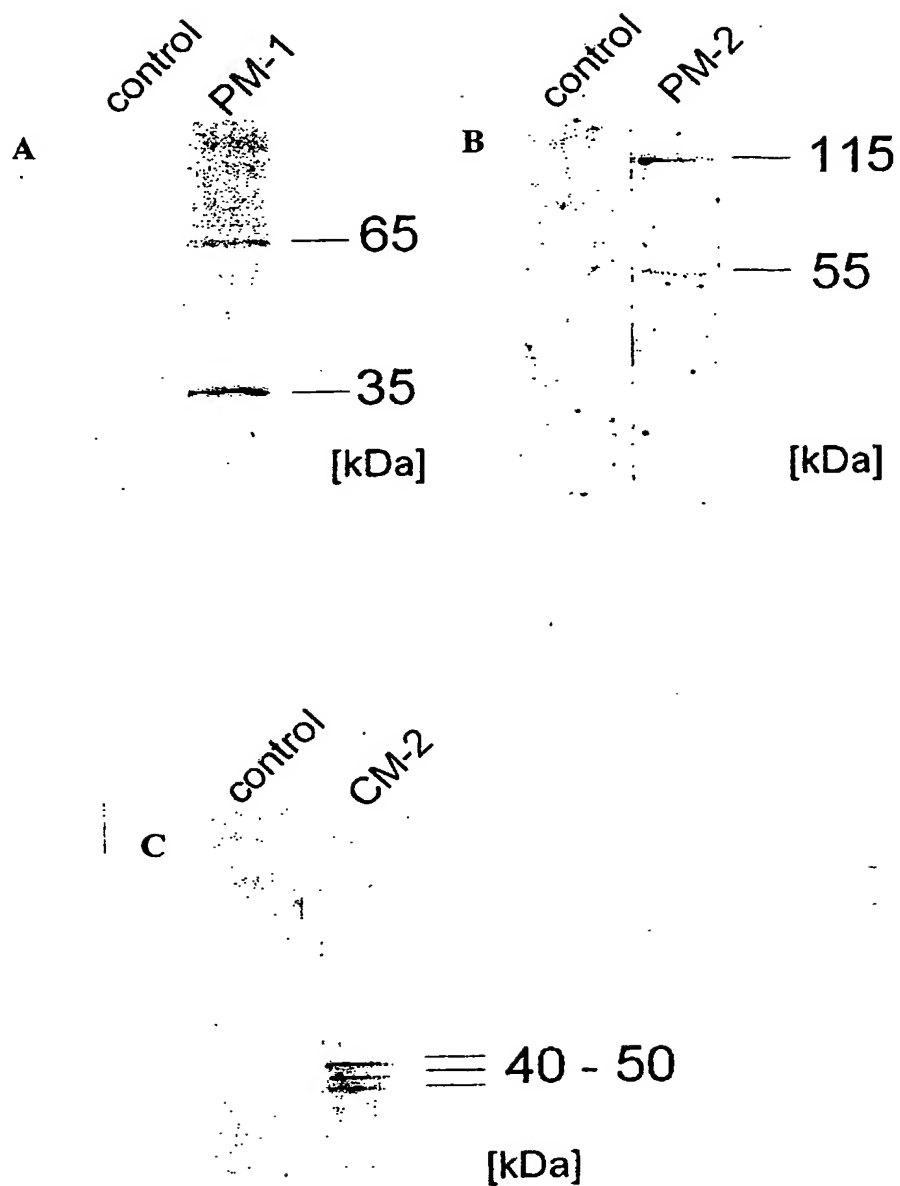


FIG. 5

BEST AVAILABLE COPY

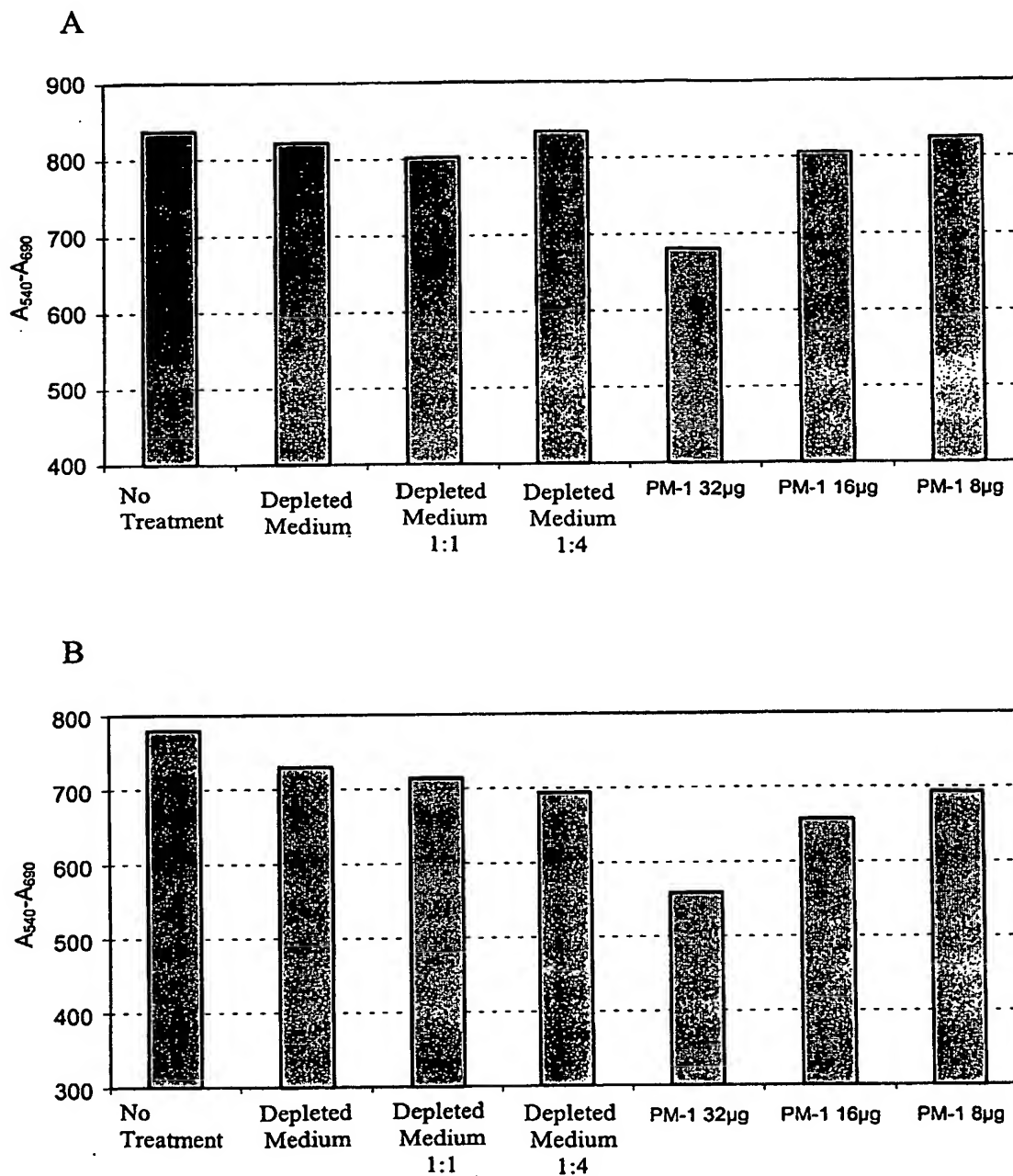


FIG. 6

BEST AVAILABLE COPY

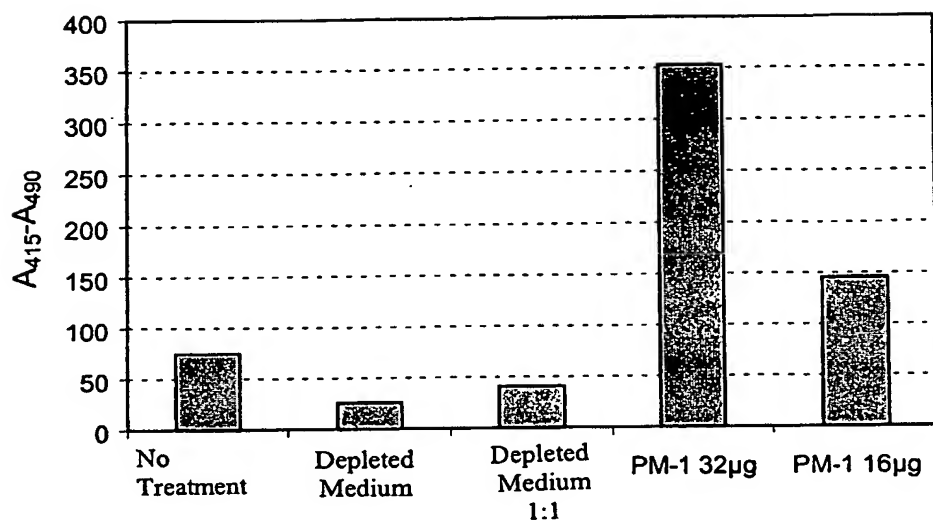


FIG. 7

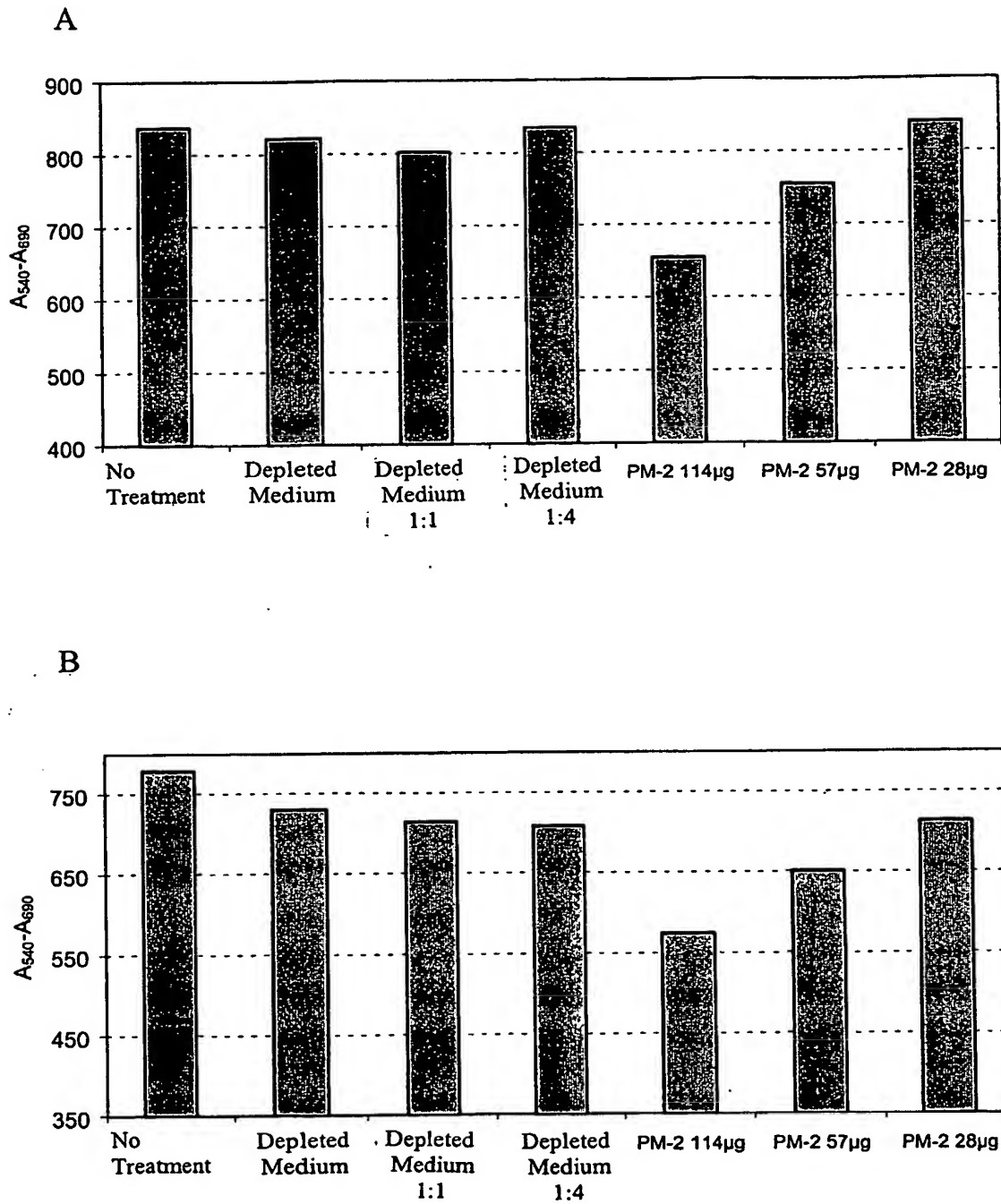


FIG. 8

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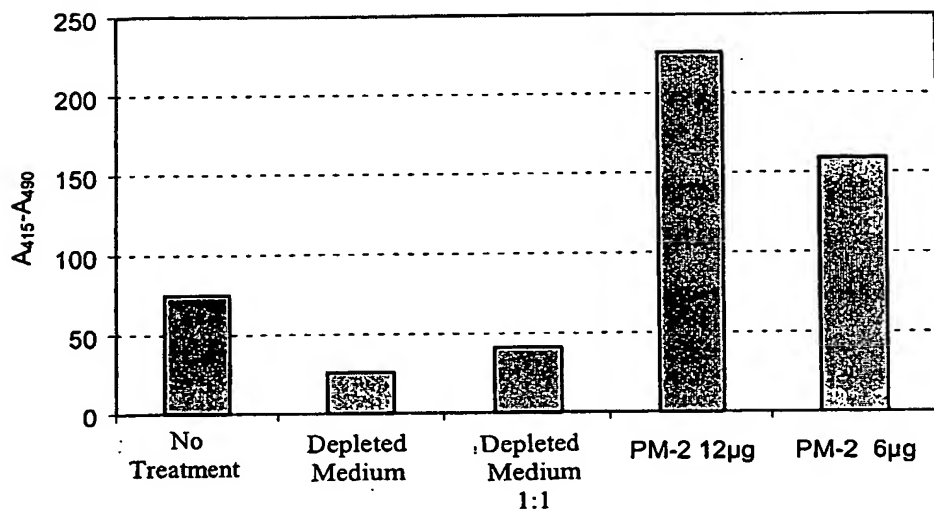


FIG. 9

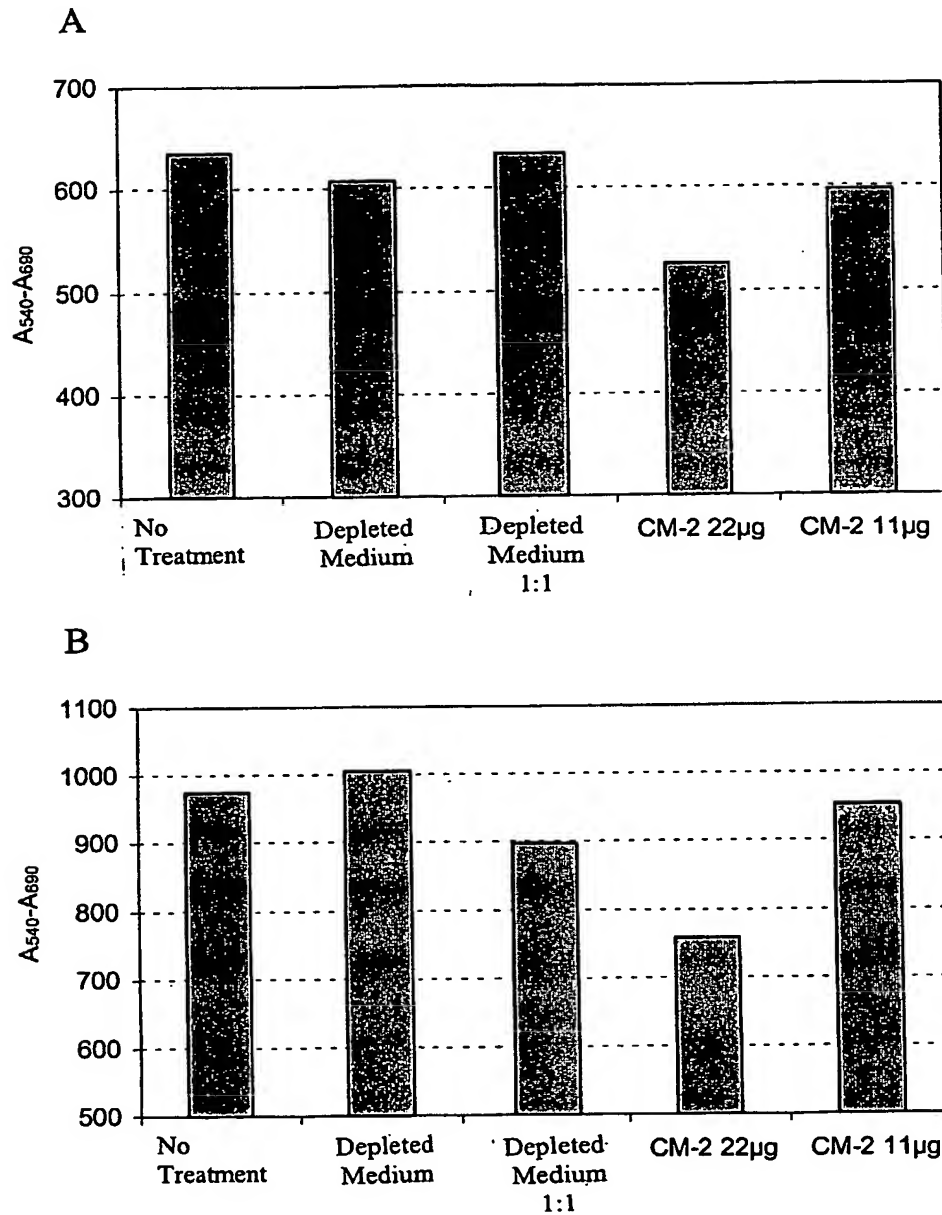


FIG. 10

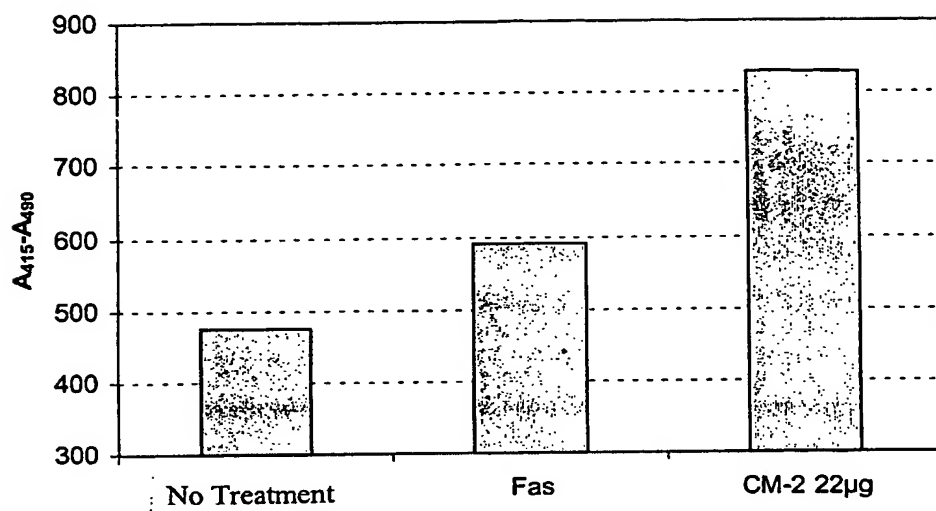


FIG. 11

PM-1 Light chain variable region sequence

tcc	tat	gtg	ctg	act	cag	cca	ccc	tcg	gtg	tca	gtg	tcc	cca	gga	caa	acg	gcc	agg	atc		60
Ser	Tyr	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ser	Pro	Gly	Gln	Thr	Ala	Arg	Ile		20
1				5					10					15							
CDR1																					
acc	tgc	tct	gga	gat	gca	ttg	cca	aaa	aaa	tat	cct	tat	tgg	tac	cag	cag	aag	tca	ggc		120
Thr	Cys	Ser	Gly	Asp	Ala	Leu	Pro	Lys	Lys	Tyr	Pro	Tyr	Trp	Tyr	Gln	Gln	Lys	Ser	Gly		40
				25					30					35							
CDR2																					
cag	gcc	cct	gtg	ctg	gtc	atc	tat	gag	gac	agc	aaa	cga	ccc	tcc	ggg	atc	cct	gag	aga		180
Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr	Glu	Asp	Ser	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg		60
				45					50					55							
ttc	tct	ggc	tcc	agc	tca	ggg	aca	atg	gcc	acc	ttg	act	atc	agt	ggg	gcc	cag	gtg	gag		240
Phe	Ser	Gly	Ser	Ser	Ser	Gly	Thr	Met	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Ala	Gln	Val	Glu		80
				65					70					75							
CDR3																					
gat	gaa	gct	gac	tac	tac	tgt	tac	tca	aca	gac	agc	agt	ggc	aat	atg	tct	tcg	gaa	ctg		300
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Tyr	Ser	Thr	Asp	Ser	Ser	Gly	Asn	Met	Ser	Ser	Glu	Leu		100
				85					90					95							
gga	cca	agc	tca	ccg	tcc																318
Gly	Pro	Ser	Ser	Pro	Ser																
				105																	

FIG. 12

PM-1 Heavy chain variable region sequence

															<u>CDR1</u>					
ggg tcc ctg aga ctc tcc tgt gca gcc tct	gga ttc acc ttt agc agc tat gcc atg agc	60																		
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser	Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser																			
1 5 10	15 20																			
															<u>CDR2</u>					
tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca gct	att agt ggt agt ggt	120																		
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly																				
25 30 35 40																				
															<u>CDR3</u>					
ggt agc aca tac tac gca gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc		180																		
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser																				
45 50 55 60																				
															<u>CDR3</u>					
aag aac acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac		240																		
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr																				
65 70 75 80																				
															<u>CDR3</u>					
tgt gcg aaa gat tca ttt cgt gaa gga ccc tgg ggc cag gga acc ctg gtc acc		294																		
Cys Ala Lys Asp Ser Phe Arg Glu Gly Pro Trp Gly Gln Gly Thr Leu Val Thr																				
85 90 95																				

FIG. 13

PM-2 Light chain variable region sequence

cag tct gcc ctg act cag cct gct tcc ctc tct gca tct cct gga gca tca gcc agt ctc	60
Gln Ser Ala Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala Ser Ala Ser Leu	
1 5 10 15 20	
<u>CDR1</u>	
acc tgc acc ttg cgc agt ggc atc aat gtt ggt acc tac agg ata tac tgg tac cag cag	120
Thr Cys Thr Leu Arg Ser Gly Ile Asn Val Gly Thr Tyr Arg Ile Tyr Trp Tyr Gln Gln	
25 30 35 40	
<u>CDR2</u>	
aag cca ggg agt cct ccc cag tat ctc ctg agg tac aaa tca gac tca gat aag cag aag	180
Lys Pro Gly Ser Pro Pro Gln Tyr Leu Leu Arg Tyr Lys Ser Asp Ser Asp Lys Gln Lys	
45 50 55 60	
ggc tct gga gtc ccc agc cgc ttc tct gga tcc aaa gat gct tcg gcc aat gca ggg att	240
Gly Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile	
65 70 75 80	
<u>CDR3</u>	
tta ctc atc tct ggg ctc cag tct gag gat gag gct gac tat tac tgt atg att tgg cac	300
Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Met Ile Trp His	
85 90 95 100	
agc agc gct tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt	348
Ser Ser Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly	
105 110 115	

FIG. 14

PM-2 Heavy chain variable region sequence

CDR1																		60
ggg tcc ctg aga ctc tcc tgt gca gcc tct	gga ttc acc ttt agc agc tat gcc atg agc																	
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser	Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser	20																
1	5	10	15															
CDR2																		120
tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca gct	att agt ggt agt ggt																	
Trp val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp val Ser Ala	Ile Aer Gly Ser Gly	40																
	25	30	35															
CDR3																		180
ggt agt aca tac tac gca gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aat tcc																		
Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser		60																
	45	50	55															
CDR4																		240
aag aac acg ctg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac																		
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr		80																
	65	70	75															
CDR5																		300
tgt gcg aaa ggt ggg gcc gaa ggc tgg tac gag tac tac tac tac tac ggt atg gac gtc																		
Cys Ala Lys Gly Gly Ala Glu Gly Trp Tyr Glu Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val		100																
	85	90	95															
CDR6																		321
tgg ggc caa ggg acc ctg gtc																		
Trp Gly Gln Gly Thr Leu Val																		
	105																	

FIG. 15

CM-2 Light chain variable region sequence

cag tct gcc ctg act cag cct gcc tcc gtg tct ggg tct cct gga cag tcg atc acc atc	60
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln Ser Ile Thr Ile	
1 5 10 15 20	
CDR1	
tcc tgc act gga acc agc agt gac gtt ggt ggt tat aac tat gtc tcc tgg tac caa cag	120
Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr Gln Gln	
25 30 35 40	
CDR2	
cac cca ggc aaa gcc ccc aaa ctc atg att tat gat gtc agt aat cgg ccc tca ggg gtt	180
His Pro Gly Lys Ala Pro Lys Leu Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val	
45 50 55 60	
tct aat cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc tct gga ctc	240
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu	
65 70 75 80	
CDR3	
cag gct gag gac gag gct gat tac tac tgc agc tca aaa aga agc agc aac act cta gta	300
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Lys Arg Ser Ser Asn Thr Leu Val	
85 90 95 100	
ttc ggc gga ggg acc aag ctg acc gtc cta	330
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu	
105 110	

FIG. 16

CM-2 Heavy chain variable region sequence

															CDR1					
aaa aag ccc ggg gag tct ctg agg atc tcc tgt aag ggc tct gga	tac agt ttt acc acc	60																		
Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Thr																				
1 5 10 15 20																				
tac tgg atc ggc tgg gtg cgc cag atg ccc ggg aaa ggc ctg gag tgg atg ggg atc atc		120																		
Tyr Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile																				
25 30 35 40																				
CDR2																				
tat cct ggt gac tct gat acc aga tac agc ccg tcc ttc caa ggc cag gtc acc atc tca		180																		
Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser																				
45 50 55 60																				
gcc gac acg tcc atc agt acc gcc tac ctg cag tgg agc agc ctg aag gcc tcg gac acc		240																		
Ala Asp Thr Ser Ile Ser Thr Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr																				
65 70 75 80																				
CDR3																				
gcc ata tat tac tgt gcg agg gag gtc tat act ggc cga aac tac tac tac tac ggt ctg		300																		
Ala Ile Tyr Tyr Cys Ala Arg Glu Val Tyr Thr Gly Arg Asn Tyr Tyr Tyr Tyr Gly Leu																				
85 90 95 100																				
gac gtc tgg ggc caa gga acc ctg gtc		327																		
Asp Val Trp Gly Gln Gly Thr Leu Val																				
105																				

FIG. 17